



Figure 1:
Delta-6 Desaturase Sequence Alignment:
Consensus key (see documentation for details)
* - single, fully conserved residue
: - conservation of strong groups
. - conservation of weak groups
- no consensus

CLUSTAL W (1.81) multiple sequence alignment

Mucor-D6	-----
Rhizopus-D6	-----
Malpina-D6	-----
Sdiclina-D6	-----
Phytium-D6	-----
Phaeo-D6	-----
Physcomit-D6	MVFAGGGLQGSLEENIDVEHIASMSLFSDFFSYVSSVGSWSVHSIQPLKRLTSKKRVS
Ceratodon-D6	MVSQGGGLSQGSIEENIDVEHLATMPLVSDFLNVGLGTLGQWSLSLSTTFAFKRLTTKKHSS
C.elegansD6	-----
Borage-D6	-----
Human-D6	-----
Mucor-D6	-----MSSDVGATVPHFYTRAEIADIHQDV-----L-DKKPEAR
Rhizopus-D6	-----MSTSDRQSV---FTLKELELINQKH-----R-DGDKSAMK
Malpina-D6	-----MAAAPSVRT---FTRAEIILNAEALN-----EGKKDAEAPF

Sdiclina-D6
Phytium-D6
Phaeo-D6
Physcomit-D6
Ceratodon-D6
C.elegansD6
Borage-D6
Human-D6

-----MVQ--GQKAEK--ISWAT-----IREHNRQDNA
-----MVD--LKPGVKRLVSWKE-----IREHATPATA
-----MGKGGDARAS--KGSTAARKISWQE-----VKTHASPEDA
ESAAVQCISAEVQRNSSTQTAELAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDC
D-----ISVEAQKESVARGPVENISQVAQPIRRRRWVQDKPVTYSLKDVASHDMPQDC
-----MVVDKNASGLR
-----MAAQIKKIYITSDE-----LKNHDKPGDL
-----MGKGGNQGEAAAREVSVPTFSWEE-----IQKHNLRTDR

Mucor-D6
Rhizopus-D6
Malpina-D6
Sdiclina-D6
Phytium-D6
Phaeo-D6
Physcomit-D6
Ceratodon-D6
C.elegansD6
Borage-D6
Human-D6

LIVVENKVYDITDFVFDHPGGERVLLTQEGRDATDVFFHEMPPS--AYELLANCYVVDCE
FIIDRKVYDVTEFLEDHPGGAQVLLTHVGKDASDVFFHAMHPES--AYEILNNYFVGDVK
LMIIDNKVYDVREFVPDHPGGS-VILTHVGKDGTDVDTFFHPEA--AWETLANFYVGDID
WIVIHKKVYDISAFE-DHPGGV-VMFTQAGEDATDAFAVFPSS--ALKLLEQYVVGDDVD
WIVIHKKVYDISKWD-SHPGGS-VMLTQAGEDATDAFAVFPSS--ALKLLEQYVVGDDVD
WIIHSNKVYDVSNNWH-EHPGGA-VIFTHAGDDMTDIFAAFHAPG--SQSLMKKFYIGELL
WIVVKNKVYDVSNFADHPGGS-VISTYFGRDGTDFSSFHAAAS--TWKILQDFYIGDVE
WIIIEKVYDVSTFAEQHPGGT-VINTYFGRDATDVSTFHAST--SWKILQNFYIGNLV
MKVDGKWLVLSEELVKKHPGGA-VIEQYRNSDATHIFAFHEGSSQAYKQLDLLKKHGEH
WISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDFAFAFPAS--TWKNLDKFFTGYL
WLVIDRKVYNITKWSIQHPGGQRVIGHYAGEDATDAFAFHDPDLEFVGKFLKPLLIGELA
*

: : : : :
: : : : :
: : : : :

Mucor-D6
Rhizopus-D6
Malpina-D6
Sdiclina-D6

PKLPIDSTDKKALNSA-----AFAQEIRDLRLDKLEKQGYFDASTGFYIYKV
-----DAHVKETPSA-----QFASEMRQLRDQLKKEGYFHSSKAYYVYKV
-----ESDRAIKND-----DFAAEVRKLRTLFSQSLGYDSSKAYYAFKV
-----QSTAAVDTS--ISDEVKKSQ-----SDFIASYRKLRLLEVKRLGLYDSSKLYLYLYKC

Phytium-D6	-----ETSKAEIEGEPASDEERARRINEFIASYRRLRVKVGMLYDASALYYAWKL
Phaeo-D6	-----PETTGKEPQQ-----IAFEKGYRDLRSKLIMMGFKSNKWFYVYKC
Physcomit-D6	-----RVEPTP-----ELLKDFREMRALFLREQLFKSSKLYYVMKL
Ceratodon-D6	-----REEPTL-----ELLKEYRELRALFLREQLFKSSKSYLFKT
C.elegansD6	DEFLEKQLEKRLDKVDINVSAYDVSVAQEKKMVESFEKLRQKLHDDGLMKANETYFLFKA
Borage-D6	-----KDYSVS-----EVSKDYRKLVFEFSKMGLYDKKGHIMFATL
Human-D6	P-----EEPSQDHGKN-----SKITEDFRALRKTAEDMNLFKTNHVFFLLLL

Mucor-D6	STTLVCIVGLAILKAWGRESTLAVFIAASLVGLFWQCGWLAHDYAHYQVIKDPNVNNL
Rhizopus-D6	LSTLALCAAGLTLLYAGHTSTLAVVASAIIVGIFWQCGWLAHDEGHHCFFEDRSWNDV
Malpina-D6	SNLCIWGLSTFIVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVFQDRFWGDL
Sdiclina-D6	ASTLSIALVSAAICLHFD--STAMYMVAAVILGLFYQCGWLAHDFLHHQVFENHLFGDL
Phytium-D6	VSTFGIAVLMAICFFFN--SFAMYMVAGVIMGLFYQCGWLAHDFLHNQVCENRTLGNL
Phaeo-D6	LSNMAIWAACALVFYSD--RFVWHLASAVMLGTFQCGWLAHDFLHHQVFTKRKHGDL
Physcomit-D6	LTNVAIFAASIAIICWSK--TISAVLASACMMALCFQCGWLSHDFLHNQVFETRNLNEV
Ceratodon-D6	LINVSIVATSIASISLYK--SYRAVLLSASLMGLFIQCGWLSHDFLHHQVFETRNLNDV
C.elegansD6	ISTLSIMAFAFYLYLG-----WYITSACLLALAWQQFGWLTHEFCHQOQPTKNRPLNDT
Borage-D6	CFIAMLFAMSVYGVLFCEG--VIVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKF
Human-D6	AHIIALESIAWFTVFYFGN-GWIPTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNHL

Mucor-D6	FLVTFGNLVQGFSLSWWKNKHNTHHASTNVSGE-----DPDIDTAPILLWDEFAVANE
Rhizopus-D6	LVVFLGNFCQGFSLSWWKNKHNTHHASTNVHGH-----DPDIDTAPVLLWDEYASAA
Malpina-D6	FGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGE-----DPDIDTHPLLTWSEHALEME
Sdiclina-D6	VGVMVGNLWQGFVSQWWKNKHNTHHAI PNLHATPEIAFHGDPDIDTMPILAWSLKMAQ--
Phytium-D6	IGCLVGNAWQGFVSQWWKNKHNHLHHA VPNLHSAKDEGFIGDPDIDTMPILLAWSKEMAR--

Physcomit-D6	R-----LLEKGTVLPHYFWFVGTAACYLLP--GWKPLVWMAVTELMGMLLGFVFLSH
Ceratodon-D6	K-----LLERGTMALHYIWFNSVAFYLLP--GWKPVVWVMVSELMSGFLLGYVFLSH
C.elegansD6	YKVYQRNAFWEQATIVGHWAVFYQLFLLPT--WPLRVAYFIIISQMGGLLIAHVVTFNH
Borage-D6	-KRNVSYRAHELGLCLVFSIWYPLLVSCLPN---WGERIMFVIASLSVTGMQVQVQFSLNH
Human-D6	---IVHKNWVDLAWAVSYIIRFFITYIPFYG--ILGALLFLNFIRFLESHWFVWVTQMNH
	: . : *
Mucor-D6	NGMPVYSPEEАНTEFYELQCITGRDVN-----CTVFGDWLMGGLNYQIEHHLFPEMPRH
Rhizopus-D6	NGMPVITEEKAESMEFFEIQVITGRDVT-----LSPLGDWFMGGLNYQIEHHVFPNMPRH
Malpina-D6	NGMPVISKEEAVDMDFFTKQIITGRDVH-----PGLFANWFTGGLNYQIEHHLFPSMPRH
Sdiclina-D6	NGMEVFDKD--SKPDFWKQLQVLSTRNVT-----SSLWIDWFMGGLNYQIDHHLFFPMVPRH
Phytium-D6	NGMSVYERE--TKPDFWQLQVTTTRNIR-----ASVMDWFTGGLNYQIDHHLFFPLVPRH
Phaeo-D6	NGMATYNAD--ARPDFWKQLQVTTTRNVTTGGHGFPAQVDFWFCGGLQYQVDDHHLFPSLPRH
Physcomit-D6	NGMEVYN-----SSKEFVSAQIVSTRDIK-----GNIFNDWFTGGLNRQIEHHLFPPTMPRH
Ceratodon-D6	NGMEVYN-----TSKDFVNAQIASTRDIK-----AGVNDWFTGGLNRQIEHHLFPPTMPRH
C.elegansD6	NSVDKYPANSRILNNFAALQILTTTRNMT-----PSPFIDWLWGGLNYQIEHHLFPPTMPRC
Borage-D6	FSSSVYVGK-PKGNWFEKQTDGTLDIS-----CPPWMDWFHGGGLQFQIEHHLFPKMPRC
Human-D6	IVMEIDQEA---YRDWFSSQLTATCNVE-----QSFNDWFSGHLNFQIEHHLFPPTMPRH
	:: * : : * * * : * : * : * :
Mucor-D6	HL SKVKSMVKPIAQKYNIPYHDTTVIGGTIEVLQTLDFVQ---KISQKFSKKML-----
Rhizopus-D6	NLPKVKPMVKSCLKKYDINYHDTGFLKGTLEVLKTLDIS---KLSLQLSKKSF-----
Malpina-D6	NFSKIQPAVETLCKKYGVRYHTTGMIEGTAEVFSRLNEVS---KAASKMGKAQ-----
Sdiclina-D6	NLPALNVLSLCKQYDIPYHETGFIAGMAEVVHLERIS---IEFFKEFPAM-----
Phytium-D6	NLPKVNVLKSLCKEFDIPFHETGFWEGLYEVVDHLADIS---KEFITTEFPAM-----
Phaeo-D6	NLAKTHALVESFCKEWGVQYHEADLVDGTMEVLHHLGSAGEFVVDVFRDGPAM-----
Physcomit-D6	NLNKIAPRVEVFCCKHGLVYEDVSIATGTCKVLKALKEVAE---AAAEQHATTS-----

Ceratodon-D6	NLNKISPHVETLCKKHGLVYEDVSMASGTYRVLTKTKDVAD---	AASHQQLAAS-----
C.elegansD6.	NLNACVKYVKEWCKENNLPLYLVDDYFDGYAMNLQQLKNMA-----	EHIQAKAA-----
Borage-D6	NLRKISPYVIELCKKHNLPPYNYASFSSKANEMTLRTRLRNTALQARDITKPLPKNLVWEALH	
Human-D6	NLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKSGKLWLDAYLHKNLLE-----	
	: :	: . . . *
Mucor-D6	---	
Rhizopus-D6	---	
Malpina-D6	---	
Sdiclina-D6	---	
Phytium-D6	---	
Phaeo-D6	---	
Physcomit-D6	---	
Ceratodon-D6	---	
C.elegansD6	---	
Borage-D6	THG	
Human-D6	---	

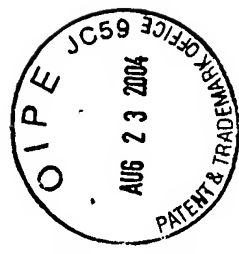


Figure 2:
Comparison of nucleotide sequence of *S. diclina* $\Delta 6$ -desaturase versus *Pythium irregulare* $\Delta 6$ -desaturase:

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	9148	Length:	1383
Ratio:	6.717	Gaps:	3
Percent Similarity:	68.948	Percent Identity:	68.948

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

S. diclina-D6 x *Pythium irregulare*-D6

```
1 ATGGTCCAGGGGCAAAAAGGCCGAGAAAGATCTCG.....TGGGCGACCAT 44
||||| | | | | | | | | | | | | | | | | | | | | | | | | |
1 ATGGTGGACCTCAAGCCTGGAGTGAAGCGCCTGGTGAGCTGGAAGGAGAT 50
45 CCGTGAGCACAAACCGCCAAAGACAAACGCGTGGATCGTGATCCACCAAGG 94
||| ||||| | | | | | | | | | | | | | | | | | | | | | | |
51 CCGCGAGCACGCGACGCCCGCGACCGCGTGGATCGTGATTCACCAAGG 100
95 TGTACGACATCTCGGCCTTTGAGGACCAACCGGGCGGCGTCGTATGTTTC 144
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 TCTACGACATCTCCAAGTGGGACTCGCACCCGGGTGGCTCCGTGATGCTC 150
145 ACGCAGGCCGGGGAAGACGCGACCGGATGCGTTCGCTGTCTTCCACCCGAG 194
```

```

|||||
151 ACGAGCGCGGAGGACGCCACGGACGCCCTTCGGGTCTTCCACCCGTC 200
|||||
195 CTCGGCGCTCAAGCTCCTCGAGCAGTACTACGTGGCGACGTCGACCACT 244
|||||
201 CTCGGCGCTCAAGCTGCTCGAGCAGTTCTACGTGGCGACGTCGGACGAAA 250
|||||
245 CGACGGCGCGCTCGACACGTCGATCTCGGACGAGGTCAAGAAAGAGCCAG 294
| | |||| | | | ||| | | | | | | | |
251 CCTCCAAGCCGAGATCGAGGGGAGCCGGCGAGCGACGAGGAGCGCGCG 300
|||||
295 .....TCGGACTTCATTGCGTCTACCGCAAGCTGCGCCT 329
|| |||| |||| |||| |||| |||| |
301 CGCCGCGAGCGCATCAACGAGTTCATCGCGTCTACCGTCTGCGCGT 350
|||||
330 TGAAGTCAAGCGCCTCGGCTTGACGACTCGAGCAAGCTCTACTACCTCT 379
| |||| | | | |||| | ||| |||| |||| |
351 CAAGTCAAGGCGCATGGGGCTCTACGACGCCAGCGCGCTCTACTACGCGT 400
|||||
380 ACAAGTGGCCCTCGACGCTGAGCATTGCGCTTGTCGGCGGCCATTGTC 429
|| | ||| | |||| ||| | | ||| ||| |||
401 GGAAGCTCGTGAGCACGTTTCGGCATCGCGGTGCTCTCGATGGCGATCTGC 450
|||||
430 CTCCACTTTGACTCGACGGCCATGTACATGGTCGGCGCTGTCATCCTTGG 479
|| ||| || |||| |||| |||| | ||| | ||
451 TTCTTCTCAACAGTTTCGCCATGTACATGGTCGGCGCGTGATTATGGG 500
|||||
480 CCTCTTTTACCAGCAGTGGGCTGGCTCGCCCATGACTTCTGCACCACC 529
|||| | |||| ||| | |||| | | |||| |||| |||
501 GCTCTTCTACCAGCAGTCCGGATGGCTGGCGCACGACTTCTTGACAACC 550
|||||
530 AAGTGTGAGAAACCCTTGTGTTGGCGACCTCGTCGGCGTCAATGGTCGGC 579
| |||| |||| | | ||| |||| |||| | | |||
551 AGGTGTGCGAGAACCGCAGCTCGGCAACCTTATCGGCTGCCTCGTGGGC 600

```


998 GCGTGGCATACTTCCTCATGGGCCAGGCGTCTCGGGCTTGCTCCTGGCG 1047
 1030 ATGGTCTTTAGCGTCGGCCACAACGGCATGGAGGTCTTTGACAAGGACAG 1079
 1048 CTGGTGTTCAGTATTGGCCACAACGGCATGTCGGGTACGAGCGCGAAAC 1097
 1080 CAAGCCCGATTTTTGAAGCTGCAAGTGCTCTCGACGGCGCAACGTGACGT 1129
 1098 CAAGCCGGACTTCTGGCAGCTGCAGGTGACCCACGACGGCGCAACATCCGCG 1147
 1130 CGTCGCTCTGGATCGACTGGTTCAATGGGGCGGCTCAAACTACCAGATCGAC 1179
 1148 CGTCGGTATTCAATGGACTGGTTCAACCGGTGGCTTGAACCTACCAGATCGAC 1197
 1180 CACCACCTTGTTCCCGATGGTGCCCGCGGCACAAACCTCCCGCGCTCAACGT 1229
 1198 CATCACCTGTTCCCGCTCGTGCCCGCGCCACAACCTGCCAAAGGTCAACGT 1247
 1230 GCTCGTCAAGTCGCTCTGCAAGCAGTACGACATCCCATAACCCAGAGACGG 1279
 1248 GCTCATCAAGTCGCTATGCAAGGAGTTCGACATCCCGTCCACGAGACCG 1297
 1280 GCTTCATCGCGGGCATGGCCGAGGTGCTCGTGCACCTCGAGCGCATCTCG 1329
 1298 GCTTCTGGGAGGGCATCTACGAGGTGCTGGACCACCTGGCGGACATCAGC 1347
 1330 ATCGAGTCTTCAAGGAGTTTCCCGCCCATGTAA 1362
 1348 AAGGAATTCAACCGAGTTCCCGAGCGGATGTAA 1380

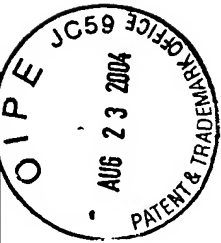


Figure 3:

Comparison of amino acid sequence of $\Delta 6$ -desaturases from *S. diclina* and *P. irregulare*

Query= *S. diclina* $\Delta 6$ -desaturase

Subject: *Pythium Irregulare* $\Delta 6$ -desaturase

>gi|16033736|gb|AF419296.1|AF419296 *Pythium irregulare* delta-6 fatty acid desaturase
mRNA, complete cds
Length = 1380

Score = 548 bits (1412), Expect = e-154

Identities = 267/449 (59%), Positives = 328/449 (73%), Gaps = 5/449 (1%)

Frame = +1

Query: 10 ISWATIREHNRQDNAWIVIIHHKVYDISAFEDHPGGVVMFTQAGEDATDAFAVFPSSALK 69

+SW IREH AWIVIIHHKVYDIS ++ HPGG VM TQAGEDATDAFAVFPSSALK

Sbjct: 34 VSWKEIREHATPATAWIVIIHHKVYDISKWDSPGGSVMLTQAGEDATDAFAVFPSSALK 213

Query: 70 LLEQYVVGVDVDQSTAAV--DTSISDEVKKSQ---SDFIASYRKLRLEVKRXXXXXXXXXX 124

LLEQ+YVGVDVD+++ A SDE + + ++FIASYR+LR++VK

Sbjct: 214 LLEQFYVGVDVDETSKAEIEGEPASDEERARRERINEFIASYRRLRVKVGKMGGLYDASALY 393

Query: 125 XXXXCASLTSLIALVSAICLHFDSTAMYMVAAILGLFYQQCGWLAHDFLHHQVFENHLF 184

ST IA++S AIC F+S AMYMVA VI+GLFYQQ GWLAHDFLH+QV EN

Sbjct: 394 YAWKLVSTFGIAVLMSAICFFFNFSFAMYMVAGVIMGLFYQQSGWLAHDFLHNQVCENRTL 573

Query: 185 GDLVGVVGNLWQGFVSQVWKNKHNTHHAIPNLHATPEIAFHGDDPDIDTMPILAWSLKMA 244
G+L+G +VGN WQGFVSQVWKNKHN HHA+PNLH+ + F GPDIDTMP+LAWS +MA
Sbjct: 574 GNLIGCLVGNWQGFVSQVWKNKHNHLHHAVPNLHSAKDEGFIGDDPDIDTMPILAWSKEMA 753

Query: 245 QHAVDSPVGLFFMRYQAYLYFPILLFARISWVIQSAMYAFYNVGPGGTFDKVQYPLLERA 304
+ A +S G FF+R QA+LYFP+LL AR+SW+ QS Y F G FDKV++ E+A
Sbjct: 754 RKAFAHAGPFFIRNQAFLYFPILLARLSWLAQSFFYVFTFEFS-FGIFDKVEFDGPEKA 930

Query: 305 XXXXXXXXXXXXXAANMSLLQAAAFLEVSQAACGLFLAMVFSVGHNGMEVFDKDSKPDF 364
NMSL + A+ + QASCG L LA+VFS+GHNGM V+++++KPDF
Sbjct: 931 GLIVHYIWQLAIPYFCNMMSLFEQVAYFLMGQAACGLLLALVFSIGHNGMSVYERETKPDF 1110

Query: 365 WKLQVLSTRNVTSLSLWIDWFMGGLNYQIDHHLFPMVPRHNLPALNVLSLCKQYDIPYH 424
W+LQV +TRN+ +S+++DWF GGLNYQIDHHLFP+VPRHNL +NVL+KSLCK++DIP+H
Sbjct: 1111WQLQVTTTRNIRASVFMDFWTGGLNYQIDHHLFPLVPRHNLPKVNVLIKSLCKEFDIPFH 1290

Query: 425 ETGFIAGMAEVVVHLERISIEFFEKEFPAM 453
ETGF G+ EVV HL IS EF EFPAM
Sbjct: 1291ETGFWEGIYEVVDHLADISKEFITEFPAM 1377